

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/044,696DATE: 01/15/99
TIME: 13:06:12

INPUT SET: S30786.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: BARCHFELD, GAIL
6 DEL GIUDICE, GIUSEPPE
7 RAPPUOLI, RINO
8
9 (ii) TITLE OF INVENTION: DETOXIFIED MUTANTS OF BACTERIAL
10 ADP-RIBOSYLATING TOXINS AS PARENTERAL ADJUVANTS
11
12 (iii) NUMBER OF SEQUENCES: 4
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: CHIRON CORPORATION, INTELLECTUAL PROPERTY -
16 R440
17 (B) STREET: P.O. BOX 8097
18 (C) CITY: EMERYVILLE
19 (D) STATE: CALIFORNIA
20 (E) COUNTRY: USA
21 (F) ZIP: 94662-8097
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: US 09/044,696
31 (B) FILING DATE: 18-MAR-1998
32 (C) CLASSIFICATION:
33
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: US 60/041,227
36 (B) FILING DATE: 21-MAR-1997
37
38 (viii) ATTORNEY/AGENT INFORMATION:
39 (A) NAME: HARBIN, ALISA A.
40 (B) REGISTRATION NUMBER: 33,895
41 (C) REFERENCE/DOCKET NUMBER: 1393.002
42
43 (ix) TELECOMMUNICATION INFORMATION:
44 (A) TELEPHONE: (510) 655-8730
45 (B) TELEFAX: (510) 655-3542
46

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47
48 (2) INFORMATION FOR SEQ ID NO:1:
49
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 711 base pairs
52 (B) TYPE: nucleic acid
53 (C) STRANDEDNESS: single
54 (D) TOPOLOGY: linear
55
56 (ii) MOLECULE TYPE: DNA (genomic)
57
58
59 (ix) FEATURE:
60 (A) NAME/KEY: CDS
61 (B) LOCATION: 1..708
62
63
64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
65
66 AAT GGC GAC AGA TTA TAC CGT GCT GAC TCT AGA CCC CCA GAT GAA ATA 48
67 Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
68 1 5 10 15
69
70 AAA CGT TTC CGG AGT CTT ATG CCC AGA GGT AAT GAG TAC TTC GAT AGA 96
71 Lys Arg Phe Arg Ser Leu Met Pro Arg Gly Asn Glu Tyr Phe Asp Arg
72 20 25 30
73
74 GGA ACT CAA ATG AAT ATT AAT CTT TAT GAT CAC GCG AGA GGA ACA CAA 144
75 Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr Gln
76 35 40 45
77
78 ACC GGC TTT GTC AGA TAT GAT GAC GGA TAT GTT TCC ACT TCT CTT AGT 192
79 Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser
80 50 55 60
81
82 TTG AGA AGT GCT CAC TTA GCA GGA CAG TAT ATA TTA TCA GGA TAT TCA 240
83 Leu Arg Ser Ala His Leu Ala Gly Gln Tyr Ile Leu Ser Gly Tyr Ser
84 65 70 75 80
85
86 CTT ACT ATA TAT ATC GTT ATA GCA AAT ATG TTT AAT GTT AAT GAT GTA 288
87 Leu Thr Ile Tyr Ile Val Ile Ala Asn Met Phe Asn Val Asn Asp Val
88 85 90 95
89
90 ATT AGC GTA TAC AGC CCT CAC CCA TAT GAA CAG GAG GTT TCT GCG TTA 336
91 Ile Ser Val Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu
92 100 105 110
93
94 GGT GGA ATA CCA TAT TCT CAG ATA TAT GGA TGG TAT CGT GTT AAT TTT 384
95 Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe
96 115 120 125
97
98 GGT GTG ATT GAT GAA CGA TTA CAT CGT AAC AGG GAA TAT AGA GAC CGG 432
99 Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg

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100      130      135      140
101
102 TAT TAC AGA AAT CTG AAT ATA GCT CCG GCA GAG GAT GGT TAC AGA TTA      480
103 Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu
104 145      150      155      160
105
106 GCA GGT TTC CCA CCG GAT CAC CAA GCT TGG AGA GAA GAA CCC TGG ATT      528
107 Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile
108      165      170      175
109
110 CAT CAT GCA CCA CAA GGT TGT GGA GAT TCA TCA AGA ACA ATC ACA GGT      576
111 His His Ala Pro Gln Gly Cys Gly Asp Ser Ser Arg Thr Ile Thr Gly
112      180      185      190
113
114 GAT ACT TGT AAT GAG GAG ACC CAG AAT CTG AGC ACA ATA TAT CTC AGG      624
115 Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg
116      195      200      205
117
118 GAA TAT CAA TCA AAA GTT AAG AGG CAG ATA TTT TCA GAC TAT CAG TCA      672
119 Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser
120      210      215      220
121
122 GAG GTT GAC ATA TAT AAC AGA ATT CGG GAT GAA TTA TGA      711
123 Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
124 225      230      235
125
126

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

137
138 Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
139   1           5           10           15
140
141 Lys Arg Phe Arg Ser Leu Met Pro Arg Gly Asn Glu Tyr Phe Asp Arg
142      20           25           30
143
144 Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr Gln
145      35           40           45
146
147 Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser
148      50           55           60
149
150 Leu Arg Ser Ala His Leu Ala Gly Gln Tyr Ile Leu Ser Gly Tyr Ser
151      65           70           75           80
152

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153  Leu Thr Ile Tyr Ile Val Ile Ala Asn Met Phe Asn Val Asn Asp Val
154                      85                      90                      95
155
156  Ile Ser Val Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu
157                      100                      105                      110
158
159  Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe
160                      115                      120                      125
161
162  Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg
163                      130                      135                      140
164
165  Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu
166  145                      150                      155                      160
167
168  Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile
169                      165                      170                      175
170
171  His His Ala Pro Gln Gly Cys Gly Asp Ser Ser Arg Thr Ile Thr Gly
172                      180                      185                      190
173
174  Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg
175                      195                      200                      205
176
177  Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser
178  210                      215                      220
179
180  Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
181  225                      230                      235
182

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..720

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAT GAT GAT AAG TTA TAT CGG GCA GAT TCT AGA CCT CCT GAT GAA ATA

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206	Asn	Asp	Asp	Lys	Leu	Tyr	Arg	Ala	Asp	Ser	Arg	Pro	Pro	Asp	Glu	Ile	
207				240					245					250			
208																	
209	AAG	CAG	TCA	GGT	GGT	CTT	ATG	CCA	AGA	GGA	CAG	AGT	GAG	TAC	TTT	GAC	96
210	Lys	Gln	Ser	Gly	Gly	Leu	Met	Pro	Arg	Gly	Gln	Ser	Glu	Tyr	Phe	Asp	
211			255					260					265				
212																	
213	CGA	GGT	ACT	CAA	ATG	AAT	ATC	AAC	CTT	TAT	GAT	CAT	GCA	AGA	GGA	ACT	144
214	Arg	Gly	Thr	Gln	Met	Asn	Ile	Asn	Leu	Tyr	Asp	His	Ala	Arg	Gly	Thr	
215			270				275					280					
216																	
217	CAG	ACG	GGA	TTT	GTT	AGG	CAC	GAT	GAT	GGA	TAT	GTT	TCC	ACC	TCA	ATT	192
218	Gln	Thr	Gly	Phe	Val	Arg	His	Asp	Asp	Gly	Tyr	Val	Ser	Thr	Ser	Ile	
219	285					290					295					300	
220																	
221	AGT	TTG	AGA	AGT	GCC	CAC	TTA	GTG	GGT	CAA	ACT	ATA	TTG	TCT	GGT	CAT	240
222	Ser	Leu	Arg	Ser	Ala	His	Leu	Val	Gly	Gln	Thr	Ile	Leu	Ser	Gly	His	
223					305					310					315		
224																	
225	TCT	ACT	TAT	TAT	ATA	TAT	GTT	ATA	GCC	ACT	GCA	CCC	AAC	ATG	TTT	AAC	288
226	Ser	Thr	Tyr	Tyr	Ile	Tyr	Val	Ile	Ala	Thr	Ala	Pro	Asn	Met	Phe	Asn	
227				320					325					330			
228																	
229	GTT	AAT	GAT	GTA	TTA	GGG	GCA	TAC	AGT	CCT	CAT	CCA	GAT	GAA	CAA	GAA	336
230	Val	Asn	Asp	Val	Leu	Gly	Ala	Tyr	Ser	Pro	His	Pro	Asp	Glu	Gln	Glu	
231			335					340					345				
232																	
233	GTT	TCT	GCT	TTA	GGT	GGG	ATT	CCA	TAC	TCC	CAA	ATA	TAT	GGA	TGG	TAT	384
234	Val	Ser	Ala	Leu	Gly	Gly	Ile	Pro	Tyr	Ser	Gln	Ile	Tyr	Gly	Trp	Tyr	
235			350				355					360					
236																	
237	CGA	GTT	CAT	TTT	GGG	GTG	CTT	GAT	GAA	CAA	TTA	CAT	CGT	AAT	AGG	GGC	432
238	Arg	Val	His	Phe	Gly	Val	Leu	Asp	Glu	Gln	Leu	His	Arg	Asn	Arg	Gly	
239	365					370					375					380	
240																	
241	TAC	AGA	GAT	AGA	TAT	TAC	AGT	AAC	TTA	GAT	ATT	GCT	CCA	GCA	GCA	GAT	480
242	Tyr	Arg	Asp	Arg	Tyr	Tyr	Ser	Asn	Leu	Asp	Ile	Ala	Pro	Ala	Ala	Asp	
243					385					390					395		
244																	
245	GGT	TAT	GGA	TTG	GCA	GGT	TTC	CCT	CCG	GAG	CAT	AGA	GCT	TGG	AGG	GAA	528
246	Gly	Tyr	Gly	Leu	Ala	Gly	Phe	Pro	Pro	Glu	His	Arg	Ala	Trp	Arg	Glu	
247				400					405				410				
248																	
249	GAG	CCG	TGG	ATT	CAT	CAT	GCA	CCG	CCG	GGT	TGT	GGG	AAT	GCT	CCA	AGA	576
250	Glu	Pro	Trp	Ile	His	His	Ala	Pro	Pro	Gly	Cys	Gly	Asn	Ala	Pro	Arg	
251			415					420					425				
252																	
253	TCA	TCG	ATC	AGT	AAT	ACT	TGC	GAT	GAA	AAA	ACC	CAA	AGT	CTA	GGT	GTA	624
254	Ser	Ser	Ile	Ser	Asn	Thr	Cys	Asp	Glu	Lys	Thr	Gln	Ser	Leu	Gly	Val	
255			430				435					440					
256																	
257	AAA	TTC	CTT	GAC	GAA	TAC	CAA	TCT	AAA	GTT	AAA	AGA	CAA	ATA	TTT	TCA	672
258	Lys	Phe	Leu	Asp	Glu	Tyr	Gln	Ser	Lys	Val	Lys	Arg	Gln	Ile	Phe	Ser	

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SEQUENCE VERIFICATION REPORT
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Original Text